

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/816,697

DATE: 04/06/2001

TIME: 10:31:45

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\04062001\I816697.raw

ENTERED

3 <110> APPLICANT: Lorenz, M., et al.
 5 <120> TITLE OF INVENTION: A NOVEL P-SELECTIN GLYCOPROTEIN LIGAND (PSGL-1)
 6 BINDING PROTEIN AND USES THEREFOR
 8 <130> FILE REFERENCE: GFN-5380
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/816,697
 C--> 11 <141> CURRENT FILING DATE: 2001-03-23
 13 <150> PRIOR APPLICATION NUMBER: 60/192,104
 14 <151> PRIOR FILING DATE: 2000-03-24
 16 <160> NUMBER OF SEQ ID NOS: 4
 18 <170> SOFTWARE: PatentIn Ver. 2.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 951
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Homo sapiens
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (1)..(948)
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 31 Met Ala Ser Pro Glu His Pro Gly Ser Pro Gly Cys Met Gly Pro Ile
 32 1 5 10 15
 34 acc cag tgc acg gca agg acc cag cag gaa gca cca gcc act ggc ccc 96
 35 Thr Gln Cys Thr Ala Arg Thr Gln Gln Glu Ala Pro Ala Thr Gly Pro
 36 20 25 30
 38 gac ctc ccg cac cca gga cct gac ggg cac tta gac aca cac agt ggc 144
 39 Asp Leu Pro His Pro Gly Pro Asp Gly His Leu Asp Thr His Ser Gly
 40 35 40 45
 42 ctg agc tcc aac tcc agc atg acc acg cgg gag ctt cag cag tac tgg 192
 43 Leu Ser Ser Asn Ser Ser Met Thr Thr Arg Glu Leu Gln Gln Tyr Trp
 44 50 55 60
 46 cag aac cag aaa tgc cgc tgg aag cac gtc aaa ctg ctc ttt gag atc 240
 47 Gln Asn Gln Lys Cys Arg Trp Lys His Val Lys Leu Leu Phe Glu Ile
 48 65 70 75 80
 50 gct tca gct cgc atc gag gag aga aaa gtc tct aag ttt gtg gtg tac 288
 51 Ala Ser Ala Arg Ile Glu Glu Arg Lys Val Ser Lys Phe Val Val Tyr
 52 85 90 95
 54 caa atc atc gtc atc cag act ggg agc ttt gac aac aac aag gcc gtc 336
 55 Gln Ile Ile Val Ile Gln Thr Gly Ser Phe Asp Asn Asn Lys Ala Val
 56 100 105 110
 58 ctg gaa cgg cgc tat tcc gac ttc gcg aag ctc cag aaa gcg ctg ctg 384
 59 Leu Glu Arg Arg Tyr Ser Asp Phe Ala Lys Leu Gln Lys Ala Leu Leu
 60 115 120 125
 62 aag acg ttc agg gag gag atc gaa gac gtg gag ttt ccc agg aag cac 432
 63 Lys Thr Phe Arg Glu Glu Ile Glu Asp Val Glu Phe Pro Arg Lys His
 64 130 135 140
 66 ctg act ggg aac ttc gct gag gag atg atc tgt gag cgt cgg cgc gcc 480
 67 Leu Thr Gly Asn Phe Ala Glu Glu Met Ile Cys Glu Arg Arg Arg Ala

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68 145          150          155          160
70 ctg cag gag tac ctg ggc ctg ctc tac gcc atc cgc tgc gtg cgc cgc 528
71 Leu Gln Glu Tyr Leu Gly Leu Leu Tyr Ala Ile Arg Cys Val Arg Arg
72          165          170          175
74 tcc cgg gag ttc ctg gac ttc ctc acg cgg ccg gag ctg cgc gag gct 576
75 Ser Arg Glu Phe Leu Asp Phe Leu Thr Arg Pro Glu Leu Arg Glu Ala
76          180          185          190
78 ttc ggc tgc ctg cgg gcc ggc cag tac ccg cgc gcc ctg gag ctg ctg 624
79 Phe Gly Cys Leu Arg Ala Gly Gln Tyr Pro Arg Ala Leu Glu Leu Leu
80          195          200          205
82 ctg cgc gtg ctg ccg ctg cag gag aag ctc acc gcc cac tgc cct gcg 672
83 Leu Arg Val Leu Pro Leu Gln Glu Lys Leu Thr Ala His Cys Pro Ala
84          210          215          220
86 gcc gcc gtc ccg gcc ctg tgc gcc gtg ctg ctg tgc cac cgc gac ctc 720
87 Ala Ala Val Pro Ala Leu Cys Ala Val Leu Leu Cys His Arg Asp Leu
88 225          230          235          240
90 gac cgc ccc gcc gag gcc ttc gcg gcc gga gag agg gcc ctg cag cgc 768
91 Asp Arg Pro Ala Glu Ala Phe Ala Ala Gly Glu Arg Ala Leu Gln Arg
92          245          250          255
94 ctg cag gcc cgg gag ggc cat cgc tac tat gcg cct ctg ctg gac gcc 816
95 Leu Gln Ala Arg Glu Gly His Arg Tyr Tyr Ala Pro Leu Leu Asp Ala
96          260          265          270
98 atg gtc cgc ctg gcc tac gcg ctg gcc aag gac ttc gtg act ctg cag 864
99 Met Val Arg Leu Ala Tyr Ala Leu Gly Lys Asp Phe Val Thr Leu Gln
100          275          280          285
102 gag agg ctg gag gag agc cag ctc cgg agg ccc acg ccc cga gcc atc 912
103 Glu Arg Leu Glu Glu Ser Gln Leu Arg Arg Pro Thr Pro Arg Gly Ile
104          290          295          300
106 acc ctg aag gag ctc act gtg cga gaa tac ctg cac tga 951
107 Thr Leu Lys Glu Leu Thr Val Arg Glu Tyr Leu His
108 305          310          315
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112 <211> LENGTH: 316
113 <212> TYPE: PRT
114 <213> ORGANISM: Homo sapiens
116 <400> SEQUENCE: 2
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118 1 5 10 15
120 Thr Gln Cys Thr Ala Arg Thr Gln Gln Glu Ala Pro Ala Thr Gly Pro
121 20 25 30
123 Asp Leu Pro His Pro Gly Pro Asp Gly His Leu Asp Thr His Ser Gly
124 35 40 45
126 Leu Ser Ser Asn Ser Ser Met Thr Thr Arg Glu Leu Gln Gln Tyr Trp
127 50 55 60
129 Gln Asn Gln Lys Cys Arg Trp Lys His Val Lys Leu Leu Phe Glu Ile
130 65 70 75 80
132 Ala Ser Ala Arg Ile Glu Glu Arg Lys Val Ser Lys Phe Val Val Tyr
133 85 90 95
135 Gln Ile Ile Val Ile Gln Thr Gly Ser Phe Asp Asn Asn Lys Ala Val

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136          100          105          110
138 Leu Glu Arg Arg Tyr Ser Asp Phe Ala Lys Leu Gln Lys Ala Leu Leu
139          115          120          125
141 Lys Thr Phe Arg Glu Glu Ile Glu Asp Val Glu Phe Pro Arg Lys His
142          130          135          140
144 Leu Thr Gly Asn Phe Ala Glu Glu Met Ile Cys Glu Arg Arg Arg Ala
145 145          150          155          160
147 Leu Gln Glu Tyr Leu Gly Leu Leu Tyr Ala Ile Arg Cys Val Arg Arg
148          165          170          175
150 Ser Arg Glu Phe Leu Asp Phe Leu Thr Arg Pro Glu Leu Arg Glu Ala
151          180          185          190
153 Phe Gly Cys Leu Arg Ala Gly Gln Tyr Pro Arg Ala Leu Glu Leu Leu
154          195          200          205
156 Leu Arg Val Leu Pro Leu Gln Glu Lys Leu Thr Ala His Cys Pro Ala
157          210          215          220
159 Ala Ala Val Pro Ala Leu Cys Ala Val Leu Leu Cys His Arg Asp Leu
160 225          230          235          240
162 Asp Arg Pro Ala Glu Ala Phe Ala Ala Gly Glu Arg Ala Leu Gln Arg
163          245          250          255
165 Leu Gln Ala Arg Glu Gly His Arg Tyr Tyr Ala Pro Leu Leu Asp Ala
166          260          265          270
168 Met Val Arg Leu Ala Tyr Ala Leu Gly Lys Asp Phe Val Thr Leu Gln
169          275          280          285
171 Glu Arg Leu Glu Glu Ser Gln Leu Arg Arg Pro Thr Pro Arg Gly Ile
172          290          295          300
174 Thr Leu Lys Glu Leu Thr Val Arg Glu Tyr Leu His
175 305          310          315
178 <210> SEQ ID NO: 3
179 <211> LENGTH: 34
180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
186 <400> SEQUENCE: 3
187 atactgaatt ccgcctctcc cgcaagggcc acat
190 <210> SEQ ID NO: 4
191 <211> LENGTH: 33
192 <212> TYPE: DNA
193 <213> ORGANISM: Artificial Sequence
195 <220> FEATURE:
196 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
198 <400> SEQUENCE: 4
199 atacaggatc cagagtgagc taagggagga aag

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/816,697

DATE: 04/06/2001

TIME: 10:31:46

Input Set : A:\seqlist.txt

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date